

Figure 1:

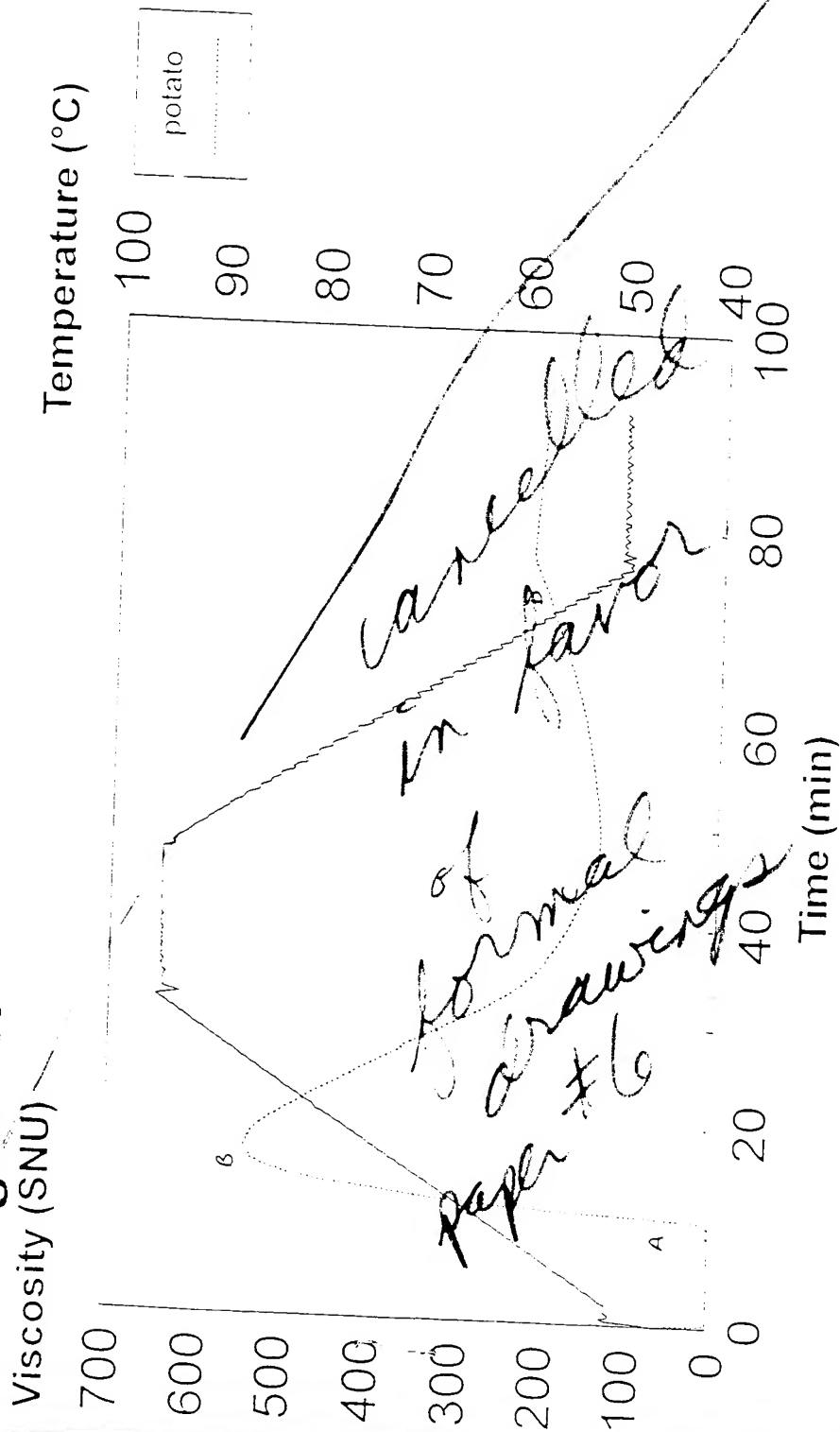
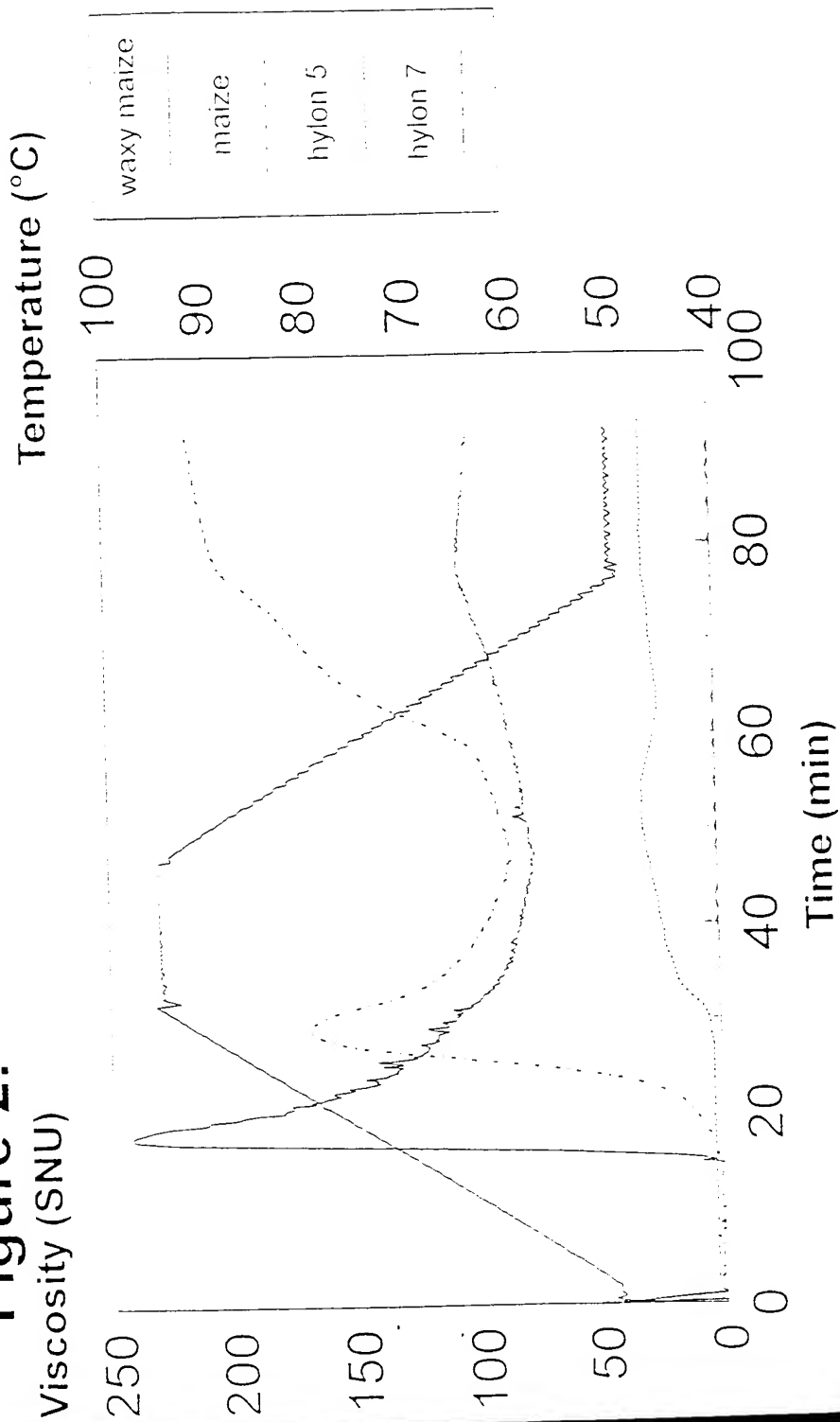
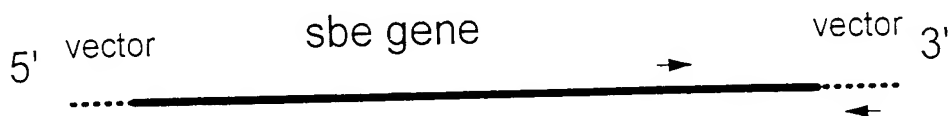


Figure 2:



NH₂

COOH

protein alignment
design primer

PCR library

850 bp

screen library

1200 bp

1500 bp

RACE

190 bp

150 bp

450 bp

750 bp

1400 bp

[illegible][illegible]

Sequence	Position	Frequency
01 X X S I - R	1	100
1 G A V E P I I S	2	100
2 D A S A G R I I A V A I I G E I S P A I S I 0 V K A S R A S S E I D E I A I A G G E K G W K T A R R P S U D I E	3	100
3 D D R I I R G G	4	100
4 D D R I I R G G	5	100
5 D D R I I R G G	6	100
6 D D R I I R G G	7	100
7 D D R I I R G G	8	100
8 D D R I I R G G	9	100
9 D D R I I R G G	10	100
10 D D R I I R G G	11	100
11 D D R I I R G G	12	100
12 D D R I I R G G	13	100
13 D D R I I R G G	14	100
14 D D R I I R G G	15	100
15 D D R I I R G G	16	100
16 D D R I I R G G	17	100
17 D D R I I R G G	18	100
18 D D R I I R G G	19	100
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22 D D R I I R G G	23	100
23 D D R I I R G G	24	100
24 D D R I I R G G	25	100
25 D D R I I R G G	26	100
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27 D D R I I R G G	28	100
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35 D D R I I R G G	36	100
36 D D R I I R G G	37	100
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46 D D R I I R G G	47	100
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50 D D R I I R G G	51	100
51 D D R I I R G G	52	100
52 D D R I I R G G	53	100
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54 D D R I I R G G	55	100
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56 D D R I I R G G	57	100
57 D D R I I R G G	58	100
58 D D R I I R G G	59	100
59 D D R I I R G G	60	100
60 D D R I I R G G	61	100
61 D D R I I R G G	62	100
62 D D R I I R G G	63	100
63 D D R I I R G G	64	100
64 D D R I I R G G	65	100
65 D D R I I R G G	66	100
66 D D R I I R G G	67	100
67 D D R I I R G G	68	100
68 D D R I I R G G	69	100
69 D D R I I R G G	70	100
70 D D R I I R G G	71	100
71 D D R I I R G G	72	100
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73 D D R I I R G G	74	100
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75 D D R I I R G G	76	100
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77 D D R I I R G G	78	100
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79 D D R I I R G G	80	100
80 D D R I I R G G	81	100
81 D D R I I R G G	82	100
82 D D R I I R G G	83	100
83 D D R I I R G G	84	100
84 D D R I I R G G	85	100
85 D D R I I R G G	86	100
86 D D R I I R G G	87	100
87 D D R I I R G G	88	100
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89 D D R I I R G G	90	100
90 D D R I I R G G	91	100
91 D D R I I R G G	92	100
92 D D R I I R G G	93	100
93 D D R I I R G G	94	100
94 D D R I I R G G	95	100
95 D D R I I R G G	96	100
96 D D R I I R G G	97	100
97 D D R I I R G G	98	100
98 D D R I I R G G	99	100
99 D D R I I R G G	100	100

This image shows a vertical strip of a document page. It contains a dense, repeating pattern of small, stylized symbols or characters, possibly a barcode or a decorative border. The symbols are arranged in a regular, grid-like fashion, with some larger, more complex symbols interspersed among the smaller ones. The overall appearance is that of a highly detailed, textured surface.

1170
 1180
 C L P D E I P Y N S I H Y O P P E S E R Y I F D - R R P K K

XmnI

1280
 1290
 P K E L R I Y E S - I G M S S P E P K I N S Y V N F R D E V

Hind III

1350
 1360
 L P R I K K L G Y N A L G I M A I O E H S Y Y A S F G Y H V

1440
 1450
 T N F F A P S S R F G T P D D L K S L I O K A H E L G I V V

1530
 1540
 L M O I V H S H A S N N T L D G L N M F D C T D S C Y F H S

SacI

1620
 1630
 G A R G Y H W M W D S R L F N Y G N W E V L R Y L L S N A R

1710
 1720
 K W L D A F K F D G F R F D G V T S M M Y I H H G L S V G F

Hinc II

1800
 1810
 T G N Y E E Y F G L A T C O / D A V V Y L M L / N D L I - G L

1890
 1900
 R P D A I T I G E D V S G M P T F D I R V D E G S I G P D V

1980
 1990
 R L N Y A I A D K R I E L L X X P D E D A R G D I X - T L

2070
 2080
 T N F F A S E Y O I E Y A E S - D D A L X D X T A F W L

Fig 5 (con) . 6/31

Page 11

2100

22.

1103

100

2340

(22)

2430

2520

26:0

§ 52 :

2700

2790

155

222

221

2000

25.

3532

SYAESHOCALVGDKTIAFWLMDKCMYDFMALDRPSTSLIDRGIALHKMIIR
 :YAESHOC::VGDKTIAFLMDK:MY: M: ::::DRGIALHKMI:
 AYAESHOC::VGDKTIAFLMDKEMYSGMSCLTDASPVVDRGIALHKMIH
 ^650 ^660 ^670
 ^680 ^690 ^700 ^710 ^720
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 : TM: LGGEGYLNFMGNEFGHPEWIDFPR GN: SYDKC
 FFTMALGGEGYLNFMGNEFGHPEWIDFPR-----EGNNWSYDKC
 ^600 ^610 ^620 ^630
 ^730 ^740 ^750 ^760 ^770
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 RR: : L: D: E: LRY: : : FDR: M: L: K: F: S: C: S: D: : : :
 RRQWNLADSEHLRYKFMNAFDRAMNSLDEKFSFLASGQIVSSMDDDNKV
 ^640 ^650 ^660 ^670 ^680
 ^780 ^790 ^800 ^810 ^820
 IVFEKGNLVFVFNHFWTKSYSDYRIACLKPGKYKVALDSDDPLFGGFGR
 : VFE: G: LVFVFNH : : Y: : Y: : C PGKY: VAL: SD: FGG GR
 VVFERGDLVFNFNHFNNTYEGYKVGCDLPGKYRVALGSDAWEFGGHGRA
 ^690 ^700 ^710 ^720 ^730
 ^830 ^840 ^850 ^860
 DHNAEYFT-----FEGWYDORPRSINVYAPCKTAVVYALVDKEEESE
 : H: : : FT E: : : RP: S: V : P : T V: Y VD: : E:
 GHVDHFTSPEGIPGVPETNFNNGRPNSFKVLSPARTCVAYYRVDERMSET
 ^740 ^750 ^760 ^770 ^780
 ^870
 EEEEEEV
 E: : : :
 EDYQTD:
 ^790

Fig 6 (con)

460 460 470 480 490
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 LNMFDCTDSCYF-HGARGYHWMWDSRLFNYSNWEVLRKLLSNARWWLD AF
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 4500 4510 4520 4530 4540
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 4550 4560 4570 4580 4590
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 4600 4610 4620 4630 4640
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 4590 4600 4610 4620 4630
 4650 4660 4670 4680 4690
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 4700 4710 4720 4730 4740
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 FPRAECHLSGGSVIPGNCF SYDKORRRFDLGDAEYLRVGLGEFDRPMQY
 FPRAECHLSGGSVIPGNCF SYDKORRRFDLGDAEYLRVGLGEFDRPMQY
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 4790 4800 4810 4820 4830
 4850 4860 4870
 4840 4850 4860

[illegible]

[illegible]

[illegible]

2795 **CTTGGTCA** **CA**ATAGAGGTTCTTGAT**-----**ATCAGTCTTGGCGGAAT**TC**ATGTGACAA**AG**GTITGGAG**TC**ATTTCCACATATAGTAG**TC**AG**GA**GATATAGG 11 con. seq
 2827 **CT**ATATAGAGGTTCTTGATGTTATCTGGCAATATTCATGTGACAG**AG**AGGTITGGCAATTTCTCCACATATAGTAGTGGAA**GA**GATATAGG 19 con. seq
 2814 **CG**ATAGAGGTTCTTGATGTTATCTGGCAATATTCATGTGACAA**AG**GTITGGCAATTTCTCCACATATAGTAGTGGAA**GA**GATATAGG 10 con. seq
 2895 **CT**ATATAGAGGTTCTTGATGTTATCTGGCAATATTCATGTGACAA**AG**GTITGGCAATTTCTCCACATATAGTAGTGGAA**GA**GATATAGG psbe2 con. seq

 2898 AGAGATGAAGTGGTGAACAAA**CA**ATGTGAAATTTATGTGCAATGCTGGGACGATCGAAATTCCTGGAGCC 11 con. seq
 2937 AGAGATGAAGTGGTGAACAAA**CA**ATGTGAAATTTATGTGCAATGCTGGGACGATCGAAATTCCTGGAG 19 con. seq
 2924 AGAGATGAAGTGGTGAACAAA**CA**ATGTGAAATTTATGTGCAATGCTGGGACGATCGAAATTCCTGGAGCC 10 con. seq
 3005 AGAGATGAAGTGGTGAACAAA**CA**ATGTGAAATTTATGTGCAATGCTGGGAC**GG****TT**CAG**AC****TTTTGGCTAGTGA**GT**CTCTGTAATTTGTCATCTCTTANA**GTAG**ACA** psbe2 con. seq

 2975 11 con. seq
 3012 19 con. seq
 3003 10 con. seq
 3123 **CCCCACTAGCAATCAATTATGTGAGACCTAAAAACAATAACCATAAATGGGAATAGTGTGATCTATGTGTTTTAA**NCNNNNNAAAAAA**AAAAAACTCGAG**

Set II

[illegible]

King II

[illegible]

Kind III

[illegible]

By:

[illegible]

Xmn I

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 CGGAATTAATGAGTATGCACATAAATCTCTACCTCAAGAGGAGCGTATTTTGGAACCCATGTACCGCCACGTTAATACCGATA
 P K L N S Y V N F R D E V L P R I K T L G Y N A V Q I M A I
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 AGTTCTGTAAAGAAATATAGATCAAAACCAATAGACAGTCTTAAAAAAGTGGTTCTGCGCAAAACCTTGGCGGTCTGGAAAT
 C E H S Y A S F S Y H Y T V F F A P S S R F G T P D O L K
 GTCTTTATATGATTAAGCTGATGAGCTAGGAAATTTGTCTCTCATGGACATTTGTACAGCCATGCATTAATTAATACCTTATATGGAC
 CAGAAATTAATATTTGAGTACTGATCTCTTAAACCAAGAGTACCTGTAAAGAGTGTGGTACGTAGTTTATATGAAATATACCTGA
 S L I D K A H E L G I V V L M D I V H S H A S N N T L O G L

Sac I

GAACATGTTTACCGGACACATACCTTTTACTTTCACTCTGGAGCTCTGGTTATCATTTGGATGTGGGATTCGCGCTCTTTAATCTAGG
 GTTGTACAAATCTGCGGTGTCTATCAACAAATGAAGTGAAGCTCGAGCACCATAAGTAACTACACCTTAAGGCGCGAGAAATTGATACC
 N M F D G T D S C Y F H S G A R G Y H W M W D S R L F N Y G
 AAATCGGAGGTACTTAGGTATCTCTCTCAAAATGCGAGATGGTGGTGGATGAGTTCAAAATTTATGGATTTAGATTTGATGGTGTAC
 TTTGACCTTCATGAATGCAATAGAAGAGAGTTACGCTCTACACCAACCTACTCAAGTTTAAACTACCTAAATCTAAACTACCAACATG
 N W E V L R Y L L S N A R W W L D E F K F D G F R F D G V -
 ATCAATGATGTATACCTACCAACGGAATATCGGTGGGATTTACTGGGAACTACGAGGAATATCTTTGACTCGCAATGATGTGGATGCTGT
 TAGTTACTACATATGAGTGGTGGCTAAATAGCCACCTTAAGTGAACCTTTGATGCTCTCTATGAACCTGAGCGTTGACTACACCTACGACA
 S M M Y T H H G L S V G F T G N Y E E Y F G L A T O V O A V

Hinc II

TATGTATCTGATGCTGTCAACGATCTTATTCACCGGCTTTTCCGAGATGCAATTTACCATTGGTGAAGATGTTACCGGAATTCGCGACAT
 ACACATAGACTACGACCGATTTCTAGAATAAGTCCCGGAAAGGGTCTACGTAAATGGTAACCACTTCTACAATCGCTTACGGCTGTAA
 V Y L M L V N D L I H G L F P D A I I I G E D V S G M P T F

Nce I

TGTATTCGGTGAAGATGGGGGTGTTGGCTTTGACTATCGGTGCATATGGCAATTTGCTGATTAATGGATTTGATTTGCTCAAGAAAGG
 AATTAAGGGGCAATTTTACCGGACAGAGCGAAATGATAGCGGAGGTATACCTTTAAGCACTATTTACCTAACTCAACGAGTCTTTTGC
 E I F V Q D G G V G F D Y R L H M A I A D K W I E L L K K R
 GGAATAGGATTTGAAGAGTGGTGTATTTTGTATACATGACAAATAGAAGATGGTGGGAAAGTGTCTTTGATTCGCTGAAGTGTATGA
 CTTACTCTTAACCTCTACCCCACTATAAGAGATATGTGACTTTTATCTTTACCAAGCGTTTGCACAAAGTATGGCACTTTGATGAT
 C E D A P V S D I V H T L T N R P W S E K D V S T A E S H C

Hinc I

TTAAGCTTATGCTGGGTGATTAAGATATAGCTATCTGGGTGATGCAAGAGGATATGTATGATTTATTTGGCTTGGATAGAGCTGTAGCTAT
 ATTTTGAAGATAGCGGATATTTTGTATGCTATAGAGGAGTACCTTTCTGATACATAGTAAATAGCGAGCTATTTGGCAATTTGAT
 C A L V D Y T A A K A L M D A D M K D F M A L D R F S T S

Acl I
Kpn I

TTTATTAATCTGTGGATGCAATTTGACATAGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTAT
 TAAATTTTGAAGATATGCTAGCGTATTTTGTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTAT
 C D F D I A L H K M I P R L T M S L D G E G L N F M G N

200

GA AAT GCGAGACGGAGA TTT GAGTGGGAGATGCGAGAA AT AAGA ACCA GGGT GCAAGAA TTT GACGGGGCTA GCGAG ATG
ACTATTTACGTC GCGCTATAAC GGACCGCTACGCTGTTA AAATGATATGGT ACCCAACGT GTTAAATGGCGGCA AGCTATAGA 2180
O K C R R R F O L G D A E Y L R Y H G L O E F O R A M O Y L

[illegible][illegible]

GGAC CAGG GATCCAACTT TGTGGGCGGAGATT GAT CAT AAT GCCGGAATA TTCACTC CTGAAGGA CG ATGA TG TCGTC
CTTGATTTT ACTAGGTGTAATAACACCGGACGCCTCTTACTCGTATTCGCCGCTAATAAGAGATTCCTAGCATATCTCGCGG 2430
C S C C P F P C U S C H I O E N A H K H I G H G E K D A B P

[illegible]

NGAAGGA ----
 -----> 253'
 AGTTTAAAT
 T T T

Fig. 9 (con)

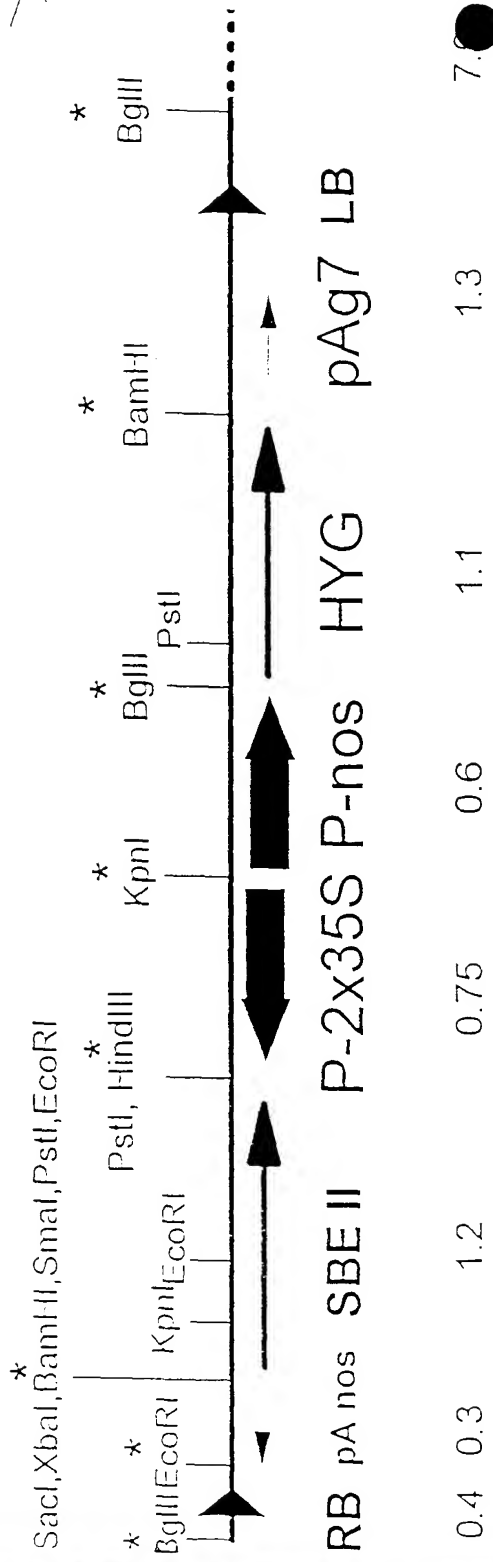


Fig. 11

Nco I
BstX I

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AGTAAATTCCTCTTTAATGATACCTCTCTAGAGTGGTAGTGGTAGTGGTACCCCTAGA 60
M P G S T T T T T T G I

EcoR I

TGGCTGAAAAGTCTCTTACAAATCCGAAATCCGACCTCTACAGTTGCAGCATCGGGGA 120
ACCGACTTTTCAGAAGAATGTTAAGGCTTAAGGCTGGAAGATGTCACCGTCTAGCCCCCT
L A E K S S Y N S E F R P S T V A A S G

AAGTCTTGTGCTGGAACCCAGAGTGATAGCTCTCATCTCTCAACAAACCAATTTGAGT 180
TTCAGGAACACGGACCTTGGGTCTCACTATCGAGGAGTAGGAGTTGTTTGGTTAAACTCA
K V L V P G T C S C S S S S S T N C F E

TCACTGAGACATCTCCAGAAAAATCCCCAGCATCAACTGATGTAGATAGTTCAACAATGG 240
AGTGACTCTGTAGAGGTCTTTTAAAGGGTCTGTAGTTGACTACATCTATCAAGTTGTTACC
F T E T S P E N S P A S T D V D S S T M

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TTGTGCGATCGGTCTAAATTTGACTCTTGTACTGCAACTCGGCAGTTCACTAGAATGTC
E H A S C I K T E N D C V E P S S D L T

GAAGTGTGAAGAGCTGGATTTTGTCTTCATCACTACAACACAAAGAAGGTGGTAAACTGG 360
CTTCACAACTTCTCGACCTAAAAACGAAGTAGTGATGTGTGATGTCTTCCACCATTTGACC
G S V E E L D F A S S L Q L C E G G K L

AGGAGTCTAAAAACATTAATACCTCTGAGAGACAAATTTGATGAATCTGATAGGATCA 420
TCTTCAGATTTTGTAAATTAAGAGACTCTCTGTTAATAACTACTTAGACTATCTAGT
E E S K T L A T S E E T I I D E S D R I

CAGAGAGGGGCTTCCCTCCACCTGGACTTGGTCAGAGATTTATGAAATAGACCCCTTT 480
CTCTCTCCCTGGTAGGGACCTGGACCTGACCCAGCTCTCTAAATACCTTTATCTGGGGGAAA
P E R C I P P P G L G C K I Y E I D P L

Hinc II

TGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAACTGAGGGAGG 540
 AGTGTGGATAGCACTTGTGGAACAAATGTCCATAAGTGTGATGTCTTTGACTCCCTCC
 L T N Y R C H L D Y R Y S C Y K K L R E

HinD III

CAATTGACAAGTATGAGGGTGGTTGGAAAGCTTTTCTCGTGGTTATGAAAAAATGGGTT 600
 GTTAACTGTTCATACTCCCAACCAACCTTCGAAAAAGAGCACCAATACTTTTTACCCAA
 A I D K Y E G G L E A F S R G Y E K M G

Pvu II

TCACTCGTAGTCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGGCCAGTCAGCTG 660
 AGTGAGCATCAAGATGTCCATAGTGAATGGCACTCACCCGAGGACCACGGGTCACTCGAC
 F T R S A T G I T Y R E W A P G A Q S A

CCCTCATTGGAGATTTCAACAATGGGACGCAAAATGCTGACATTATGACTCGGAATGAAT 720
 GGGAGTAACTCTAAAAGTTGTTAACCCCTGCGTTTACGACTGTAATACTGAGCCTTACTTA
 A L I G D F N N W D A N A D I M T R N E

TTGGTGTCTGGGAGATTTTTCTGCCAAATAATGTGGATGGTTCTCTGCAATTCCTCATG 780
 AACCACAGACCCCTCTAAAAAGACGGTTTATTACACCTACCAAGAGGACGTAAAGGAGTAC
 F G V W E I F L P N N V D G S P A I P H

SnaBI

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 CCAGGTCTCACTCTCATGCAATACCTGTGAGGTAGTCCACAAATTCCTAAGGTAAAGACGAA
 G S R V K I R M D T P S G V K C S I P A

GGATCAAGTACTCTTCACAGCTTCTGATGAAATTCATATATATGGAATATATATGATC 900
 CCTAGTTGATGAGAGGTGTGGAAGGACTACTTTAAGGTATATTTCTTATATATATATCTG
 W I N Y S S C L P D E I P Y N G I Y Y C

CACCCCAAGAGGAGAGGTATATCTTCCAAACACCCACGACCAAAAGCAAAAGTGGTGA 960
 GTGGGTCTCTCTCTCATATAGAAAGTGTGGGTGGCGGTCTTTGGTTTCAAGGAGCT
 P P E E E P Y I P C H P R P K K P K S L

GAATATATGAATCTCATAATTGGAAATGAGTAGTCCGGAGCCATAAAATTAACTCATAAGTGA
 CTATATACTTAGAGTATAACCTTACTCATCAGGCCCTGGGATTTTAATTGAGTATGCACT 1020
 R I Y E S H I G M S S P E P K I N S Y V

Xmn I

Hind III

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 TAAAACTCTACTTCAAGAGGGAGCGTATTTTTCGAACCCCATGTTACGGCCACGTTTAAT
 N F R D E V L P R I K K L G Y N A V C I

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 M A I C E H S Y Y A S F G Y H V T N F F

CACCAAGCAGCCGTTTTTGAACGCCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATG 1200
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 A P S S R F G T P D D L K S L I D K A H

Nsi I

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 E L G I V V L M D I V H S H A S N N T L

Sac I

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 TACCTGACTTGTACAAACTGCCGTGGCTATCAACAAATGAAAGTGAGACCTCGAGCACCAA
 D G L N Y F D G T D S C Y F H S G A R G

ATGATTGGATGTGGGATTCGGGCTTTTAACTATGGAAACTGGGAGGTACTTAGGTATC 1380
 TAGTAACCTACACCCATAAGGGCGGAAAAATGGATACCTTTGACCCCTGCATGAATGCATAG
 A H W M W D S P L F N Y G N W E V L R Y

TCTCTGAAATGGAGATGGTGGTGGATGAGTTGAAATTTGATGGATTTAGATTTGATG 1440
 TAGAGAGTTTACGCTCTACCAACCAACCTACCTCAAGTTTAACTACCTAAATCTAAAGTAC
 L L S N A P A W L D E F K F D G F R F D

GTGTGACATCAATGATGTATACTCACCACGGATTATCGGTGGGATTCACTGGGAACTACG
 CACACTGTAGTTACTACATATGAGTGGTCCCTAATAGCCACCCTAAGTGACCCCTGATGC
 G V T S M M Y T H H G L S V G F T G N Y 1500

Hinc II

AGGAATACCTTGGACTCGCAACTGATGTGGATGCTGTTGTGTATCTGATGCTGGTCAACG
 TCTTATGAAACCTGAGCGTTGACTACACCTACGACAAACACATAGACTACGACCACTTGC
 E E Y F G L A T D V D A V Y Y L M L V N 1560

ATCTTATTCATGGGCTTTTCCAGATGCAATTACCATTTGGTGAAGATGTTAGCGGAATGC
 TAGAATAAGTACCCGAAAAGGGTCTACGTTAATGGTAACCACTTCTACAATCGCCTTACG
 D L I H G L F P D A I T I G E D V S G M 1620

CGACATTTTGTATTCCCGTTCAAGATGGGGGGTGTGGCTTTGACTATCGGCTGCATATGG
 GCTGTAAAACATAAGGGGCAAGTTCTACCCCCACAACCGAAACTGATAGCCGACGTATAAC
 P T F C I P V Q D G G V G F D Y R L H M 1680

CAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACGGGATGAGGATTGGAGAGTGGGTG
 GTTAACGACTATTTACCTAACTCAACGAGTTCTTTGCCCTACTCCTAACCTCTCACCCAC
 A I A D K W I E L L K K R D E D W R V G 1740

ATATTGTTCAACACTGACAAATAGAAGATGGTGGGAAAAGTGTGTTTTCATACGCTGAAA
 TATAACAAGTATGTGACTGTTTATCTTCTACCAGCCTTTTTCACACAAAGTATGCGACTTT
 D I V H T L T N R R W S E K C V S Y A E 1800

GTCAATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTCTGGCTGATGGACAAGGATA
 CAGTACTAGTTGAGATCAGCCCACTATTTTGATATCGTAAGACCGACTACCTGTTCCTAT
 S H D Q A L V G D K T I A F W L M D K D 1860

TGATGATTTTATGGCTCTGGATAGACCGCCCAACATGATTAAATAGATCGTGGGATAGCAT
 AGATACATAAATACCGAGACCTATCTGGCGGTTGTAGTAATTAATAGCACCCCTATCGTA
 M Y D F M A L D R P P T S L I D P G I A 1920

Asp 718
 Kpn I

TGCATACGATGATTTAGGCTGTAACTATGGGATTAAGGAGGAGGAGGATACCTAAATTTG
 AGTGTTCTATTAATCCGAGACATTTGATACCTAATCTCTCTCTCCCATGGAATTAAGT
 L F M Y I P L Y T M G L G G E G Y L Y F 1980

EcoRI

TGGGAATGAATTGGGCCACCGTGAGTGGATTGATTTCCCTAGGGGTGAACACACCGTCT
 2040
 ACCCTTTACTTAAGCCGGTGGGAGTCACCTAACTAAAGGGATCCCGACTTGTGTGGAGA
 M G A E F G F P E W I C F P R A E C - L
 CTGATGACTCAGTAATTCGCGGAAACCAATTGAGTTATGATAAATGCAGACGGAGATTTG
 2100
 GACTACTGAGTCATTAAGGGCCCTTGGTTAAGTCAATACTATTTACGCTCGCCTCTAAAC
 S D D S V I P G N C F S Y D K C R R R F

SspI

ACCTGGGAGATGCAGAATATTTAAGATACCGTGGGTTGCAAGAATTTGAACGGGCTATGC
 2160
 TGGACCGCTCTACGTCTTATAAATTCTATGGCACCCCAACGTTCTTAAACTGGCCCGATACG
 D L G D A E Y L R Y R G L Q E F D R A M
 AGTATCTTGAAGATAAATATGAGTTTATGACTTCAGAACACCAGTTTCATATCAGGAAAGG
 2220
 TCATAGAAGCTTCTATTTTACTCAAATACTGAAGTCTTGTGGTCAAGTATAGTGCCTTTCC
 G Y L E D K Y E F M T S E H Q F I S R K
 ATGAAGGAGATAGGATGATTGTATTTGAAAAAGGAAACCTAGTTTTTGTCTTTAATTTTC
 2280
 TACTTCCTCTATCCTACTAACATAAACTTTTTCTTTGGATCAAAAACAGAAATTAAGG
 D E G D R M I V F E K G N L V F V F N F
 ACTGGACAAAAAGCTATTCAGACTATCGCATAGGCTGCCTGAAGCGCTGGAAAAATACAAGG
 2340
 TGACCTGTTTTTCGATAAGTCTGATAGCGTATCCGACGGACTTCGGACCTTTTATGTTCC
 H W T K S Y S D Y R I G C L K P G K Y K
 TTGCCTTGGACTCAGATGATCCACTTTTTGGTGGCTTCGGGAGAAATGATCATTAATGCCG
 2400
 AACGGAAACCTGAGTCTACTAGGTGAAAAACCCAGCGCGCTTTAACTAGTATTACGGC
 V A L D S D D P L F G G F G R I D H N A

SspI

ATATTTGACCTTTGAAGGATGGTATGATGATGGTCTCGTTGATTTATGGTGTATGGAC
 2460
 TTATTAAGTGGAAATTCCTACCATACTACTAGGAGGAGCAAGTTAATACCATATACGTC
 E Y F T F E G W Y D D P F P S I Y V A A

CTTGTAGAACAGCAGTGGTCTATGCACCTAGTAGACAAAGAAGAAGAAGAAGAAGAAG 2520
GAACATCTTGTGTCGTCACCAGATACGTGATCACTGTCTTCTCTCTCTCTCTCTCTCTC
P C R T A V V Y A L V D K E E E E E E E

AAGAAGAAGTAGCAGTAGTAGAGAAGAAGTAGTAGTAGAGAAGAAGAAAGAACGAACCTTGTG
 TTCTTCTTCATCGTCATCATCTTCTTCATCATCATCTTCTTCTTACTTGCTTGAACAC

30/31

